

From: Ramirez, Delia
Sent: Friday, February 03, 2006 2:32 PM
To: Jarrell, Noble
Subject: 10/675685

Hi,

I would like to request the following alignments:

1. SEQ ID NO: 3 against SEQ ID NO:7, 10 and 16
2. SEQ ID NO: 7 against SEQ ID NO:14 and 18

Thank you very much,

Delia M. Ramirez, Ph.D.
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Noble
Fm 213/06
10 PR 4AM
10 UNL gcf

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OM protein - protein search, using sw model

Run on: February 3, 2006, 15:17:20 ; Search time 0.001 seconds
 (without alignments)

Title: US-10-675-685-14
 Perfect score: 178
 Sequence: 1 VISQLLILVPLSQEQHTYATYLOSKIVALPSRWLV 36

Scoring table: BL0SUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 19 residues

Total number of hits satisfying chosen parameters: 1
 Minimum DB seq length: 0
 Maximum DB seq length: 20000000000
 Post-processing: Maximum Match 0\$
 Maximum Match 100\$
 Listing first 2 summaries

Database : Pending Parents AA Main:US-10-675-685-7
 1: /cgn2_6/ptodata/7/paa/ptctus_COMB.pep:US-10-675-685-7
 2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:US-10-675-685-7
 3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:US-10-675-685-7
 4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:US-10-675-685-7
 5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:US-10-675-685-7
 6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:US-10-675-685-7
 7: /cgn2_6/ptodata/1/paa/US077_COMB.pep:US-10-675-685-7
 8: /cgn2_6/ptodata/1/paa/US078_COMB.pep:US-10-675-685-7
 9: /cgn2_6/ptodata/1/paa/US079_COMB.pep:US-10-675-685-7
 10: /cgn2_6/ptodata/1/paa/US080_COMB.pep:US-10-675-685-7
 11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:US-10-675-685-7
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 13: /cgn2_6/ptodata/1/paa/US083_COMB.pep:US-10-675-685-7
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 25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:US-10-675-685-7
 26: /cgn2_6/ptodata/1/paa/US096_COMB.pep:US-10-675-685-7
 27: /cgn2_6/ptodata/1/paa/US097_COMB.pep:US-10-675-685-7
 28: /cgn2_6/ptodata/1/paa/US098_COMB.pep:US-10-675-685-7
 29: /cgn2_6/ptodata/1/paa/US099_COMB.pep:US-10-675-685-7
 30: /cgn2_6/ptodata/1/paa/US100_COMB.pep:US-10-675-685-7
 31: /cgn2_6/ptodata/1/paa/US101_COMB.pep:US-10-675-685-7
 32: /cgn2_6/ptodata/1/paa/US102_COMB.pep:US-10-675-685-7
 33: /cgn2_6/ptodata/1/paa/US103_COMB.pep:US-10-675-685-7
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 37: /cgn2_6/ptodata/1/paa/US107_COMB.pep:US-10-675-685-7
 38: /cgn2_6/ptodata/1/paa/US108_COMB.pep:US-10-675-685-7
 39: /cgn2_6/ptodata/1/paa/US109_COMB.pep:US-10-675-685-7
 40: /cgn2_6/ptodata/1/paa/US110_COMB.pep:US-10-675-685-7
 41: /cgn2_6/ptodata/1/paa/US111_COMB.pep:US-10-675-685-7
 42: /cgn2_6/ptodata/1/paa/US112_COMB.pep:US-10-675-685-7
 43: /cgn2_6/ptodata/1/paa/US114_COMB.pep:US-10-675-685-7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	14	7.9	19	36	US-10-675-685-7

RESULT 1 US-10-675-685-7					
; Sequence 7, Application US/10675685					
; GENERAL INFORMATION:					
; APPLICANT: Gu, Yizhong					
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E					
; CURRENT APPLICATION NUMBER: US/10/675-685					
; CURRENT FILING DATE: 2003-09-30					
; PRIOR APPLICATION NUMBER: US 60/207,456					
; PRIOR FILING DATE: 2000-05-26					
; PRIOR APPLICATION NUMBER: US 60/235,359					
; PRIOR FILING DATE: 2000-09-27					
; NUMBER OF SEQ ID NOS: 1881					
; SOFTWARE: Aeomica Sequence Listing Engine					
; SEQ ID NO: 7					
; LENGTH: 19					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
; US-10-675-685-7					
Query Match 7.9% ; Score 14 ; DB 36 ; Length 19;					
Best Local Similarity 28.6% ; Pred. No. 0 ; Matches 2 ; Conservative 3 ; Mismatches 2 ; Indels 0 ; Gaps 0 ; Gaps 0 ;					
QY 28 VALPSRW 34					
DB 11 LATLAGW 17					
Search completed: February 3, 2006, 15:17:20					
Job time : 0.001 sec					
GenCore version 5.1.6					
Copyright (C) 1993 - 2006 CompuGen Ltd.					
OM protein - protein search, using sw model					
Run on: February 3, 2006, 15:17:20 ; Search time 0.001 seconds					
(without alignment)					
0.380 Million cell updates/sec					
Title: US-10-675-685-18					
Perfect score: 105					
Sequence: 1 GQNMPAIIAGGIVLSPAYG 20					
Scoring table: BLOSUM62					

Gapop 10.0 , Gapext 0.5
 Searched: 1 seqs, 19 residues
 Total number of hits satisfying chosen parameters: 1
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 2 summaries

Database :

Pending Patents AA Main:US-10-675-685-7
 1: /cgn2_6/ptodata7_1/paa/PTCTUS COMB .pep US-10-675-685-7
 2: /cgn2_6/ptodata1_1/paa/US066_COMB .pep US-10-675-685-7
 3: /cgn2_6/ptodata1_1/paa/US073 COMB .pep US-10-675-685-7
 4: /cgn2_6/ptodata1_1/paa/US074 COMB .pep US-10-675-685-7
 5: /cgn2_6/ptodata1_1/paa/US075 COMB .pep US-10-675-685-7
 6: /cgn2_6/ptodata1_1/paa/US076 COMB .pep US-10-675-685-7
 7: /cgn2_6/ptodata1_1/paa/US077 COMB .pep US-10-675-685-7
 8: /cgn2_6/ptodata1_1/paa/US078 COMB .pep US-10-675-685-7
 9: /cgn2_6/ptodata1_1/paa/US079 COMB .pep US-10-675-685-7
 10: /cgn2_6/ptodata1_1/paa/US080 COMB .pep US-10-675-685-7
 11: /cgn2_6/ptodata1_1/paa/US081 COMB .pep US-10-675-685-7
 12: /cgn2_6/ptodata1_1/paa/US082 COMB .pep US-10-675-685-7
 13: /cgn2_6/ptodata1_1/paa/US083 COMB .pep US-10-675-685-7
 14: /cgn2_6/ptodata1_1/paa/US084 COMB .pep US-10-675-685-7
 15: /cgn2_6/ptodata1_1/paa/US085 COMB .pep US-10-675-685-7
 16: /cgn2_6/ptodata1_1/paa/US086 COMB .pep US-10-675-685-7
 17: /cgn2_6/ptodata1_1/paa/US087 COMB .pep US-10-675-685-7
 18: /cgn2_6/ptodata1_1/paa/US088 COMB .pep US-10-675-685-7
 19: /cgn2_6/ptodata1_1/paa/US089 COMB .pep US-10-675-685-7
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 22: /cgn2_6/ptodata1_1/paa/US092 COMB .pep US-10-675-685-7
 23: /cgn2_6/ptodata1_1/paa/US093 COMB .pep US-10-675-685-7
 24: /cgn2_6/ptodata1_1/paa/US094 COMB .pep US-10-675-685-7
 25: /cgn2_6/ptodata1_1/paa/US095 COMB .pep US-10-675-685-7
 26: /cgn2_6/ptodata1_1/paa/US096 COMB .pep US-10-675-685-7
 27: /cgn2_6/ptodata1_1/paa/US097 COMB .pep US-10-675-685-7
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 29: /cgn2_6/ptodata1_1/paa/US099 COMB .pep US-10-675-685-7
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 32: /cgn2_6/ptodata1_1/paa/US102 COMB .pep US-10-675-685-7
 33: /cgn2_6/ptodata1_1/paa/US103 COMB .pep US-10-675-685-7
 34: /cgn2_6/ptodata1_1/paa/US104 COMB .pep US-10-675-685-7
 35: /cgn2_6/ptodata1_1/paa/US105 COMB .pep US-10-675-685-7
 36: /cgn2_6/ptodata1_1/paa/US106 COMB .pep US-10-675-685-7
 37: /cgn2_6/ptodata1_1/paa/US111 COMB .pep US-10-675-685-7
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 41: /cgn2_6/ptodata1_1/paa/US111 COMB .pep US-10-675-685-7
 42: /cgn2_6/ptodata1_1/paa/US112 COMB .pep US-10-675-685-7
 43: /cgn2_6/ptodata1_1/paa/US114 COMB .pep US-10-675-685-7
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 45: /cgn2_6/ptodata1_1/paa/US601 COMB .pep US-10-675-685-7
 46: /cgn2_6/ptodata1_1/paa/US602 COMB .pep US-10-675-685-7
 47: /cgn2_6/ptodata1_1/paa/US603 COMB .pep US-10-675-685-7
 48: /cgn2_6/ptodata1_1/paa/US604 COMB .pep US-10-675-685-7
 49: /cgn2_6/ptodata1_1/paa/US605 COMB .pep US-10-675-685-7
 50: /cgn2_6/ptodata1_1/paa/US607 COMB .pep US-10-675-685-7
 51: /cgn2_6/ptodata1_1/paa/US608 COMB .pep US-10-675-685-7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query

No.	Score	Match	Length	DB ID	Description
1	20	19.0	19	36	US-10-675-685-7 Sequence 7, Appli

ALIGMENTS

RESULT 1
 US-10-675-685-7
 ; Sequence 7, Application US/10675685
 ; GENERAL INFORMATION:
 ; APPLICANT: Gu, Yizhong
 ; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: PBO114
 ; CURRENT APPLICATION NUMBER: US/10/675,685
 ; CURRENT FILING DATE: 2003-09-30
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; SEQ ID NO: 7
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-675-685-7

Query Match Similarity 19.0%; Score 20; DB 36; Length 19;
 Best Local Similarity 80.0%; Pred. No. 0;
 Matches 4; Conservave 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 AILAG 10
 | : |||
 Db 12 AILAG 16

Search completed: February 3, 2006, 15:17:21
 Job time : 1 secs

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OM protein - protein search, using sw model

Run on: February 3, 2006, 15:09:35 ; Search time 1 Seconds

(without alignments) 5.685 Million cell updates/sec

Title: US-10-675-685-3

Perfect score: 98.98

Sequence: 1 MMCLKILRISLAILAGWALC.....AADCDILDECTCRDPKAEEENQ 1791

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3 seqs., 3174 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Database : US10675685 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	95.4	96.6	1770 1	US-10-675-685-10
2	73.1	74.6	1385 1	US-10-675-685-16
3	94	1.0	19 1	US-10-675-685-7

ALIGNMENTS

RESULT 1

; Sequence 10, Application US/10675685

; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong

; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

; FILE REFERENCE: PB0114

; CURRENT APPLICATION NUMBER: US/10/675-685

; CURRENT FILING DATE: 2003-09-30

; PRIORITY NUMBER: US 6,0/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIORITY NUMBER: US 6,0/236,359

; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NO: 1881

; SOFTWARE: Aeonica Sequence Listing Engine

; SEQ ID NO 10

; LENGTH: 1770

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-675-685-10

Query Match	96.6%	Score 9524;	DB 1;	Length 1770;
Best Local Similarity	100.0%	Pred. No. 0;	Indels 0;	Gaps 0;
Matches 1734; Conservative	0;	Mismatches 0;		

Qy	1 MMCLKILRISLAILAGWALCANSANSELGWTMTRKKSLVEREHLNQVLEGERCWIGAKVRRPR 60
Db	1 MMCLKILRISLAILAGWALCANSANSELGWTMTRKKSLVEREHLNQVLEGERCWIGAKVRRPR 60
Qy	61 ASPQHHLFGVYPSRAGNYLRPPVYGEQEHTHTGRSKPDTEGNAVSVPDLDTEPAGLRG 120
Db	61 ASPQHHLFGVYPSRAGNYLRPPVYGEQEHTHTGRSKPDTEGNAVSVPDLDTEPAGLRG 120
Qy	121 AVEEAPAPNGDSTPQSELGLDDAYLNQRKSBSLGBAGIQKGSAMATTTAIFTTL 180
Db	121 AVEEAPAPWYGDSPQSELGLDDAYLNQRKSBSLGBAGIQKGSAMATTTAIFTTL 180
Qy	181 NEPKPETORGWAKSQRQQWKRRAEDQGDGSSHQQPWPXKSLKHKRKCSPEEESN 240
Db	181 NEPKPETORGWAKSQRQQWKRRAEDQGDGSSHQQPWPXKSLKHKRKCSPEEESN 240
Qy	241 QNGGEGSYREAFETNSQVGLPLIYPSGRGRERLLIRPEVLAIEPRAFTYEAWKPEGGON 300
Db	241 QNGGEGSYREAFETNSQVGLPLIYPSGRGRERLLIRPEVLAIEPRAFTYEAWKPEGGON 300
Qy	301 NPALIAGVFDNCSTSITSDKGWALGIRSCKDKGKRDARFFSLCTDRVKATLISHSRVQ 360
Db	301 NPALIAGVFDNCSTSITSDKGWALGIRSCKDKGKRDARFFSLCTDRVKATLISHSRVQ 360
Qy	361 PGWTWTHVAATYDGRHMALYVDGTQVASSLDQSCPLNSPEMASCRSLIQQGDSSEDGHYFR 420
Db	361 PGWTWTHVAATYDGRHMALYVDGTQVASSLDQSCPLNSPEMASCRSLIQQGDSSEDGHYFR 420
Qy	421 GHIGTLYFVNSTALPQSHFOHQSSQSSEEEATDVLVLTASREPNTWYPERDEKYPRLEV 480
Db	421 GHIGTLYFVNSTALPQSHFOHQSSQSSEEEATDVLVLTASREPNTWYPERDEKYPRLEV 480
Qy	481 LQGFPEPEBILSPLQPLCGQTVCNDVLLISQYNGWLRGERVYIYQVNNICDDGELNP 540
Db	481 LQGFPEPEBILSPLQPLCGQTVCNDVLLISQYNGWLRGERVYIYQVNNICDDGELNP 540
Qy	541 IVSBEQIRLQHEALNEAFSRYNISWQLSVHQVINSTLHRVVLVNCEPSKIGNDHCDPEC 600
Db	541 IVSEEQIRLQHEALNEAFSRYNISWQLSVHQVINSTLHRVVLVNCEPSKIGNDHCDPEC 600
Qy	661 SPKRAYMSVKEIKEALQLNSTHPLN1I PASSUREDLAGAATPWNWDKDAVTHLGGIVLSPA 720
Db	661 SPKRAYMSVKEIKEALQLNSTHPLN1I PASSUREDLAGAATPWNWDKDAVTHLGGIVLSPA 720
Qy	721 YYCAMPGHDTM1HEVGHVGLTHVFKGVSERSCNDPCKETYPSMETSQDLCADTPPKS 780
Db	721 YYCAMPGHDTM1HEVGHVGLTHVFKGVSERSCNDPCKETYPSMETSQDLCADTPPKS 780
Qy	781 ELCREPEPTSDTCGTRPGAPFTNMSYTDNCNTDNFTPNQVARYHCYLDVYQONTES 840
Db	781 ELCREPEPTSDTCGTRPGAPFTNMSYTDNCNTDNFTPNQVARYHCYLDVYQONTES 840
Qy	841 RKCPTPIPMMYQTNSLTHWLPPTSGVYDRAGSLCAGACTDGTFRQYVHTASSR 900
Db	841 RKCPTPIPMMYQTNSLTHWLPPTSGVYDRAGSLCAGACTDGTFRQYVHTASSR 900
Qy	901 RVCDSSGWTPEAVGPPDOPCBLQLANSPEVHLYHMANVTPCPTEGCSUBLFQHP 960
Db	901 RVCDSSGWTPEAVGPPDOPCBLQLANSPEVHLYHMANVTPCPTEGCSUBLFQHP 960
Qy	961 VOADTTLWVTSFEMESSQVLFDTTEILLENKESVHLGPLDTCIDPLTICLHVDFGVSGV 1020
Db	961 VOADTTLWVTSFEMESSQVLFDTTEILLENKESVHLGPLDTCIDPLTICLHVDFGVSGV 1020
Qy	1021 KYTFDERIEIDAA1LTSQPHSPPLCSGRCPRYQVRDPPFASGLPVVVTSHRKFTDVE 1080
Db	1021 KYTFDERIEIDAA1LTSQPHSPPLCSGRCPRYQVRDPPFASGLPVVVTSHRKFTDVE 1080

QY 1141 KVCPLLEGGNCVGBPSLCYMYEGDGCICPFERKTSIVDGGIYTPKGYLDQWATRAYSSH 1200
 Db 735 KVCPLLEGGNCVGBPSLCYMYEGDGCICPFERKTSIVDGGIYTPKGYLDQWATRAYSH 794
 QY 1201 DKKKCPVSIYTGEPSLICITSYHPDLNTRPLTGWFCVASENETODRSEPEGSLKKE 1260
 Db 795 DKKKCPVSIYTGEPSLICITSYHPDLNTRPLTGWFCVASENETODRSEPEGSLKKE 854
 QY 1261 DEWLKVCFTRPGEARAIFIYLTDGLVGEHQOPTTYLYTDVRSNHSLGTYGLSQCQH 1320
 Db 855 DEWLKVCFTRPGEARAIFIYLTDGLVGEHQOPTTYLYTDVRSNHSLGTYGLSQCQH 914
 QY 1321 NPLIINVTHONVLFHHTTSVLNPNSPRVGISAVALRTSSRIGLSAPSNCISEDEGONH 1380
 Db 915 NPLIINVTHONVLFHHTTSVLNPNSPRVGISAVALRTSSRIGLSAPSNCISEDEGONH 974
 QY 1381 QGQSCIHRPGKDKDSCPBLLDHDADVNCSTSIGPLAKCAITCORGPAQAOASSGQYTRPM 1440
 Db 975 QGQSCIHRPGKDKDSCPBLLDHDADVNCSTSIGPLAKCAITCORGPAQAOASSGQYTRLM 1034
 QY 1441 QREILLTSSSGHDQNVSCLPVDGVPPDSLVNANFSSEGTKFLRKCSISCVPPAKLQ 1500
 Db 1035 QREILLTSSSGHDQNVSCLPVDGVPPDSLVNANFSSEGTKFLRKCSISCVPPAKLQ 1094
 QY 1501 GLSPWLTCLEDGHWMSLPVYCKLECDAPPILNNANLILPHCLQDNHDVGTICKYECKPGY 1560
 Db 1095 GLSPWLTCLEDGHWMSLPVYCKLECDAPPILNNANLILPHCLQDNHDVGTICKYECKPGY 1154
 QY 1561 YVAEAEGRVKRNKLKIQCLEGGIWEQGSCIPVVCBPPPVPVFGMXYCTNGFSLDSOCVL 1620
 Db 1155 YVAEAEGRVKRNKLKIQCLEGGIWEQGSCIPVVCBPPPVPVFGMXYCTNGFSLDSOCVL 1214
 QY 1621 NCNQERECLPILTKEGLWTQFKLCENLQGCPPPSELNSVEYKCEQGYGIGAVCSPL 1680
 Db 1215 NCNQERECLPILTKEGLWTQFKLCENLQGCPPPSELNSVEYKCEQGYGIGAVCSPL 1274
 QY 1681 CVLPPSDPMLPBNTADTLERIWMEPVKQSIVCTGFRQWHDPVLVHJCQSCPFOANG 1740
 Db 1275 CVLPPSDPMLPBNTADTLERIWMEPVKQSIVCTGFRQWHDPVLVHJCQSCPFOANG 1334
 QY 1741 WCOTINNRAYCHYDGGDCSSTLSSKKVIFPAAADCOLDECTCRDPKAENQ 1791
 Db 1335 WCOTINNRAYCHYDGGDCSSTLSSKKVIFPAAADCOLDECTCRDPKAENQ 1385

RESULT 3
 US-10-675-685-7
 ; Sequence 7, Application US/10675685
 ; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: PB0114
 ; CURRENT APPLICATION NUMBER: US/10/675, 685
 ; PRIOR APPLICATION NUMBER: US 03-09-30
 ; PRIOR FILING DATE: 2003-05-26
 ; PRIOR APPLICATION NUMBER: US 60/207, 456
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 7
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-675-685-7

Query Match Score 94; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMCLKILRISLAILAGWAL 19

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2006, 15:10:59 ; search time 0.0119723 Seconds
 (without alignments)
 2.842 Million cell updates/sec

Title: US-10-675-685-7
 Perfect score: 94
 Sequence: 1 MMCLKILRSLAILAGWAL 19

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1791 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Listing First 1 summaries

Database : Pending_Patents_AA_Main.US-10-675-685-3

Pending_Patents_AA_Main.US-10-675-685-3

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/cgn2_6/ptodata/1/paa/US073_COMBO.pep:US-10-675-685-3

/cgn2_6/ptodata/1/paa/US074_COMBO.pep:US-10-675-685-3

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/cgn2_6/ptodata/1/paa/US076_COMBO.pep:US-10-675-685-3

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 51: /cgn2_6/ptodata/1/paa/US607_COMBO.pep:US-10-675-685-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Query Score	Match Length	DB ID
1	94	100.0	1791 36 US-10-675-685-3
SEQUENCE 3 , ALIGNMENTS			
Result 1	94	100.0	1791 36 US-10-675-685-3
SEQUENCE 3 , APPLICATION			
SEQUENCE 3 , Application US/10675685			
GENERAL INFORMATION:			
APPLICANT: Gu, Yizhong			
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E			
FILE REFERENCE: P00114			
CURRENT APPLICATION NUMBER: US/10/675_685			
CURRENT FILING DATE: 2003-09-30			
PRIOR APPLICATION NUMBER: US 60/207,456			
PRIOR FILING DATE: 2000-05-26			
PRIOR APPLICATION NUMBER: US 60/236,359			
PRIOR FILING DATE: 2000-09-27			
NUMBER OF SEQ ID NOS: 1881			
SOFTWARE: Aeomica Sequence Listing Engine			
SEQ ID NO: 3			
LENGTH: 1791			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-10-675-685-3			
Query Match Score 94; DB 16; Length 1791;			
Best Local Similarity 100.0%; Pred. No. 0; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 MMCLKILRSLAILAGWAL 19			
Db 1 MMCLKILRSLAILAGWAL 19			
Search completed: February 3, 2006, 15:11:01			
Job time : 0.0119723 secs			
GenCore version 5.1.6			
Copyright (c) 1993 - 2006 Compugen Ltd.			
Run on: February 3, 2006, 15:10:59 ; Search time 1.11531. Seconds (without alignments)			
2.842 Million cell updates/sec			
Title: US-10-675-685-10			
Perfect score: 9702			
Sequence: 1 MMCLKILRSLAILAGWAL.....HTYATYLOQSKitVALGVALC.....			
Scoring table: BLOSUM62			

Qy	601	EHPUTGYDGCRLQGRCYSWNRRDGLCRAVECNMLNDFFGCCDPOAVADVRKTCFDD	660	Qy	1681	CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734
Db	601	BHPUTGYDGCRLQGRCYSWNRRDGLCRAVECNMLNDFFGCCDPOAVADVRKTCFDD	660	Db	1681	CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734
Qy	661	SPKRAYMSVKELKEBALQINSTHFLNITYFASSVREDLAGATWFDKDATHLGIVLSPA	720	Search completed: February 3, 2006, 15:11:01			
Db	661	SPKRAYMSVKELKEBALQINSTHFLNITYFASSVREDLAGATWFDKDATHLGIVLSPA	720	Job time : 1.11531 secs			
Qy	721	YYGMPGHITDMTHBVGHLGLYHVFKGVSERESCDNPCKETVPSMETSQGDLCAADTA	780	Copyright (c) 1993 - 2006 Compugen Ltd.			
Db	721	YYGMPGHITDMTHBVGHLGLYHVFKGVSERESCDNPCKETVPSMETSQGDLCAADTA	780	GenCore version 5.1.6			
Qy	781	ELCREPEPTSDPCGFTTRPQAPTPNMSYTDNCNTDNFTPNQVARMCYLDLVYQQTES	840	OM protein - protein search, using sw model			
Db	781	ELCREPEPTSDPCGFTTRPQAPTPNMSYTDNCNTDNFTPNQVARMCYLDLVYQQTES	840	Run on: February 3, 2006, 15:10:59 ; Search time 0.872716 Seconds			
Qy	841	RKPTPIPPIPMTQGQTKSLTHWLPPISGVYDRASSLCAACTEDGTFRQVHTASSR	900	(without alignment)			
Db	841	RKPTPIPPIPMTQGQTKSLTHWLPPISGVYDRASSLCAACTEDGTFRQVHTASSR	900	2.842 Million cell updates/sec			
Qy	901	RYCDSSGGTWPEAVGPDPDOPCEPSIQLQANSPEVHLYHMNMTPCPTEGCSLELLFQHP	960	Title: US-10-675-685-16			
Db	901	RYCDSSGGTWPEAVGPDPDOPCEPSIQLQANSPEVHLYHMNMTPCPTEGCSLELLFQHP	960	Sequence: 1 MMCIKILRISLALAGWALC.....AA			
Qy	961	VQADTLTLMWTSPPMESSQVLDPETEILENKESVHGPLDTCIDPIUTKLHVDGKVSG	1020	Scoring table: BL0SUM62			
Db	961	VQADTLTLMWTSPPMESSQVLDPETEILENKESVHGPLDTCIDPIUTKLHVDGKVSG	1020	Total number of hits satisfying chosen parameters: 1			
Qy	1021	KVTFDERIEIDAAALTSQPHSPLCGQPRVYQVLRDPFPASGLPVPVVTSHRKETDVE	1080	Minimum DB seq length: 0			
Db	1021	KVTFDERIEIDAAALTSQPHSPLCGQPRVYQVLRDPFPASGLPVPVVTSHRKETDVE	1080	Maximum DB seq length: 2000000000			
Qy	1081	VTPGQMYQVTLABAGGELGEASPLHNHGAPYCGDKVSKERLGEBCDDGDLVSGPGCS	1140	Post-processing: Minimum Match 0*			
Db	1081	VTPGQMYQVTLABAGGELGEASPLHNHGAPYCGDKVSKERLGEBCDDGDLVSGPGCS	1140	Maximum Match 100*			
Qy	1141	KYCELERGFNCVGEPSLPCYMYRGDGICCEPFERKTSIVDCGTYPK3FLDONATRAYSSHE	1200	Database : Pending Patents_AA Main:US-10-675-685-3			
Db	1141	KYCELERGFNCVGEPSLPCYMYRGDGICCEPFERKTSIVDCGTYPK3FLDONATRAYSSHE	1200	1: /cgn2_6/podata/1/paa/us066_cmb..pep.us-10-675-685-3			
Qy	1201	DKKKCPVSLTSEPHSLICTSYPOLNRPLTGWPFCVASENETODDRSEOEPEGSLKKE	1260	2: /cgn2_6/podata/1/paa/us073_cmb..pep.us-10-675-685-3			
Db	1201	DKKKCPVSLTSEPHSLICTSYPOLNRPLTGWPFCVASENETODDRSEOEPEGSLKKE	1260	3: /cgn2_6/podata/1/paa/us074_cmb..pep.us-10-675-685-3			
Qy	1261	DEWLRKVCFNRGEARAIIFFLTDTGIVLPGEHQOPTVTLTIDVRSNNHSLGTYGLSCQH	1320	4: /cgn2_6/podata/1/paa/us075_cmb..pep.us-10-675-685-3			
Db	1261	DEWLRKVCFNRGEARAIIFFLTDTGIVLPGEHQOPTVTLTIDVRSNNHSLGTYGLSCQH	1320	5: /cgn2_6/podata/1/paa/us076_cmb..pep.us-10-675-685-3			
Qy	1321	NPLIINTYTHONVLPHHTTSVLPNFNSPRVGTSAVALRTSSRIGLSQH1380	1380	6: /cgn2_6/podata/1/paa/us077_cmb..pep.us-10-675-685-3			
Db	1321	NPLIINTYTHONVLPHHTTSVLPNFNSPRVGTSAVALRTSSRIGLSQH1380	1380	7: /cgn2_6/podata/1/paa/us078_cmb..pep.us-10-675-685-3			
Qy	1381	QCOSCTIHRPCGKQDSCBPSLILHDADYVNTCTS1GPGHLMKCATTCORGPAQASSGOYTRM	1440	8: /cgn2_6/podata/1/paa/us079_cmb..pep.us-10-675-685-3			
Db	1381	QCOSCTIHRPCGKQDSCBPSLILHDADYVNTCTS1GPGHLMKCATTCORGPAQASSGOYTRM	1440	9: /cgn2_6/podata/1/paa/us080_cmb..pep.us-10-675-685-3			
Qy	1441	QKBILLTCSGEWDQVNSCLPVDGVPDLSVNYANFSCEBTKELKRC1SCVPPAKLQ	1500	10: /cgn2_6/podata/1/paa/us081_cmb..pep.us-10-675-685-3			
Db	1441	QKBILLTCSGEWDQVNSCLPVDGVPDLSVNYANFSCEBTKELKRC1SCVPPAKLQ	1500	11: /cgn2_6/podata/1/paa/us082_cmb..pep.us-10-675-685-3			
Qy	1501	GLSPWLTCLEDGLWSLPEVYCKLECDAPPTILNANLPHCLQDNHVGTTICKYBCKPGY	1560	12: /cgn2_6/podata/1/paa/us083_cmb..pep.us-10-675-685-3			
Db	1501	GLSPWLTCLEDGLWSLPEVYCKLECDAPPTILNANLPHCLQDNHVGTTICKYBCKPGY	1560	13: /cgn2_6/podata/1/paa/us084_cmb..pep.us-10-675-685-3			
Qy	1561	YVAESAEGKVNKLKLIQCLREGGIWVQGSC1PVCVPPVPEGMYECTNGFSLDSQCVL	1620	14: /cgn2_6/podata/1/paa/us085_cmb..pep.us-10-675-685-3			
Db	1561	YVAESAEGKVNKLKLIQCLREGGIWVQGSC1PVCVPPVPEGMYECTNGFSLDSQCVL	1620	15: /cgn2_6/podata/1/paa/us086_cmb..pep.us-10-675-685-3			
Qy	1621	NCNOERERKLPILTCTREGLWTOEFLKLCENLQCECPPPPSELSNSVEYKEOQYGYGIGAVCSP1	1680	16: /cgn2_6/podata/1/paa/us087_cmb..pep.us-10-675-685-3			
Db	1621	NCNOERERKLPILTCTREGLWTOEFLKLCENLQCECPPPPSELSNSVEYKEOQYGYGIGAVCSP1	1680	17: /cgn2_6/podata/1/paa/us088_cmb..pep.us-10-675-685-3			
Qy	1681	CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	18: /cgn2_6/podata/1/paa/us089_cmb..pep.us-10-675-685-3			
Db	1681	CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	19: /cgn2_6/podata/1/paa/us090_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	20: /cgn2_6/podata/1/paa/us091_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	21: /cgn2_6/podata/1/paa/us092_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	22: /cgn2_6/podata/1/paa/us093_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	23: /cgn2_6/podata/1/paa/us094_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	24: /cgn2_6/podata/1/paa/us095_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	25: /cgn2_6/podata/1/paa/us096_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	26: /cgn2_6/podata/1/paa/us097_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	27: /cgn2_6/podata/1/paa/us098_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	28: /cgn2_6/podata/1/paa/us099_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	29: /cgn2_6/podata/1/paa/us100_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	30: /cgn2_6/podata/1/paa/us101_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	31: /cgn2_6/podata/1/paa/us102_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	32: /cgn2_6/podata/1/paa/us103_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	33: /cgn2_6/podata/1/paa/us104_cmb..pep.us-10-675-685-3			
Qy	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	34: /cgn2_6/podata/1/paa/us105_cmb..pep.us-10-675-685-3			
Db	1734	1681 CVIPPSDPVMLPENITADLLEHMEPVKVSIVCTGRQWHPDPVLYHCIOQSC	1734	35: /cgn2_6/podata/1/paa/us106_cmb..pep.us-10-675-685-3			
Qy	36:						

ALIGNMENTS						
Result	No.	Score	Match	Length	DB	ID
	1	7351	96.5	1791	36	US-10-675-685-3
SEQUENCE 3 , Appli						
SUMMARIES						
Query Description						
No. Score Match Length DB ID						
; RESULT 1						
; Sequence 3 , Application US/10675685						
; GENERAL INFORMATION:						
; APPLICANT: Gu, Yizhong						
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E						
; FILE REFERENCE: PH0114						
; CURRENT APPLICATION NUMBER: US/10/675,685						
; CURRENT FILING DATE: 2003-09-30						
; PRIOR APPLICATION NUMBER: US 60/207,456						
; PRIOR FILING DATE: 2000-05-26						
; PRIOR APPLICATION NUMBER: US 60/236,359						
; PRIOR FILING DATE: 2000-09-27						
; NUMBER OF SEQ ID NOS: 1881						
; SOFTWARE: Acomica Sequence Listing Engine						
; SEQ ID NO 3						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
; US-10-675-685-3						
; Query Match Score 7351; DB 36; Length 1791;						
; Best Local Similarity 96.5%; Pred. No. 0; Mismatches 7; Indels 406; Gaps 1;						
; Matches 1377; Conservative 1; Mismatches 1; Indels 406; Gaps 1;						
Qy	1	1	MNCNKIRISLALLAGWALCSANSELGTRKSLVVERHLNVLLEGERCWIGAKYRPR	60	Db	1081
Qy	1	MNCNKIRISLALLAGWALCSANSELGTRKSLVVERHLNVLLEGERCWIGAKYRPR	60	Db	1081	
Qy	61	ASQHHLFGVYPSRAGNYLRPVGVGEIHTGRSKSPDTEGNAVSLVPPDLTENPAGLR	120	Db	1141	
Db	61	ASQHHLFGVYPSRAGNYLRPVGVGEIHTGRSKSPDTEGNAVSLVPPDLTENPAGLR	120	Qy	795	
Qy	121	AVEEPAAPWGDSPIGOSBLLGDDDAYLGNQRKSKESEAGTOKGSAMAATTAAITFL	180	Db	1201	
Db	121	AVEEPAAPWGDSPIGOSBLLGDDDAYLGNQRKSKESEAGTOKGSAMAATTAAITFL	180	Qy	855	
Qy	181	NEEPKETORRGAWSKSRQRQVKRRAEDQGDSGSISSHFOQPKHSLKHGKSPPEESN	240	Db	1261	
Db	181	NEEPKETORRGAWSKSRQRQVKRRAEDQGDSGSISSHFOQPKHSLKHGKSPPEESN	240	Qy	915	

Db	1321	NPLINVTTHQNVLEHTTSPVLFNPFESSRVRGTSVAURTSRRGLSAFNSCSBDEGNH	1380
Qy	975	OQGSCIHRPGKQDSCPSLIDHADVNCSTSIGPGLMKCATTCORGPAQASSEQYIRLM	1034
Db	1381	OQGSCIHRPGKQDSCPSLIDHADVNCSTSIGPGLMKCATTCORGPAQASSEQYIRLM	1440
Qy	1035	QEILLTSGHHDQVNLSPVDCGVPPDSLNYANFSSEGTKFLKRCISCVPPAKLQ	1094
Db	1441	QEILLTSGHHDQVNLSPVDCGVPPDSLNYANFSSEGTKFLKRCISCVPPAKLQ	1500
Qy	1095	GISPWLTCIEDGLWSLPEVYCKLECDAPPILANNLIPHCLQDNHDVGTICKYECKPGY	1154
Db	1501	GISPWLTCIEDGLWSLPEVYCKLECDAPPILANNLIPHCLQDNHDVGTICKYECKPGY	1560
Qy	1155	YYAESAEKGVRNKLKKTOCLEGGIWEQSCIPYVVCBPPPVFEGMYECTNGFSLDSCQVL	1214
Db	1561	YYAESAEKGVRNKLKKTOCLEGGIWEQSCIPYVVCBPPPVFEGMYECTNGFSLDSCQVL	1620
Qy	1215	NCNQEREKLPILCTKEGLWTQFKLCENLQGCPPPPSELNSVEYKEEQGYGAVCSP	1274
Db	1621	NCNQEREKLPILCTKEGLWTQFKLCENLQGCPPPPSELNSVEYKEEQGYGAVCSP	1680
Qy	1275	CYIPPSDFMLPNITADTLIEHWMEPYKVQSIVCTGRQWHDPVLVHICQSCPFOADG	1334
Db	1681	CYIPPSDFMLPNITADTLIEHWMEPYKVQSIVCTGRQWHDPVLVHICQSCPFOADG	1740
Qy	1335	WCDTINNRAYCHYDGDDCCSSTLSSKKVTPFAADCCLDECTCRDPKAENQ	1385
Db	1741	WCDTINNRAYCHYDGDDCCSSTLSSKKVTPFAADCCLDECTCRDPKAENQ	1791

Search completed: February 3, 2006, 15:11:04
 Job time : 3.87272 secs

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Om protein - protein search, using sw mode1

Run on: February 3, 2006, 15:16:21 ; Search time 0.001 Seconds

(without alignments)
1.064 Million cell updates/sec

Title: US-10-675-685-7
Perfect score: 94
Sequence: 1 MMCLKILRISLAILAGWAL 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 56 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 2 summaries

Database : US10675685_2.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	21.3	20	1 US-10-675-685-18	Sequence 18, App1
2	14	14.9	36	1 US-10-675-685-14	Sequence 14, App1

ALIGNMENTS

RESULT 1
US-10-675-685-18
; Sequence 18, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675, 685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207, 456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236, 359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 14
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-675-685-18

Query Match 21.3%; Score 20; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AILAG 16
Db 6 AILAG 10

RESULT 2
US-10-675-685-14
; Sequence 14, Application US/10675685
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675, 685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207, 456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236, 359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 14
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-675-685-14

Query Match 14.9%; Score 14; DB 1; Length 36;
Best Local Similarity 28.6%; Pred. No. 0;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 11 LAIAGW 17
Db 28 VALPSRW 34

Search completed: February 3, 2006, 15:16:22
Job time : 0.001 secs